

RAW SEQUENCE LISTING

EFS

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Application Serial Number: 10/570,904B

Source: 1FWO

Date Processed by STIC: 1/30/07

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IFWO

RAW SEQUENCE LISTING

DATE: 01/30/2007

PATENT APPLICATION: US/10/570,904B

TIME: 08:42:54

Input Set : N:\efs\01_29_07\10570904b_efs\CorrectedSequenceListing-

3rd.txt

Output Set: N:\CRF4\01302007\J570904B.raw

3 <110> APPLICANT: TAKESHIMA, Seiji
 4 MATSUMURA, Tadanobu
 5 KISHIMOTO, Takahide
 6 OKA, Masanori
 7 HIRAYAMA, Noriaki
 9 <120> TITLE OF INVENTION: MODIFIED PYRROLOQUINOLINE QUINONE (PQQ) DEPENDENT GLUCOSE
 DEHYDROGENASE
 10 EXCELLENT IN SUBSTRATE SPECIFICITY
 12 <130> FILE REFERENCE: 251134
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/570,904B
 C--> 14 <141> CURRENT FILING DATE: 2006-03-07
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/012508
 15 <151> PRIOR FILING DATE: 2004-08-31
 17 <150> PRIOR APPLICATION NUMBER: JP 2003-315797
 18 <151> PRIOR FILING DATE: 2003-09-08
 20 <150> PRIOR APPLICATION NUMBER: JP 2003-315799
 21 <151> PRIOR FILING DATE: 2003-09-08
 23 <150> PRIOR APPLICATION NUMBER: JP 2004-060283
 24 <151> PRIOR FILING DATE: 2004-03-04
 26 <150> PRIOR APPLICATION NUMBER: JP 2004-060282
 27 <151> PRIOR FILING DATE: 2004-03-04
 29 <150> PRIOR APPLICATION NUMBER: JP 2004-151905
 30 <151> PRIOR FILING DATE: 2004-05-21
 32 <160> NUMBER OF SEQ ID NOS: 94
 34 <170> SOFTWARE: PatentIn version 3.1
 36 <210> SEQ ID NO: 1
 37 <211> LENGTH: 455
 38 <212> TYPE: PRT
 39 <213> ORGANISM: Acinetobacter baumannii
 41 <400> SEQUENCE: 1
 43 Asp Ile Pro Leu Thr Pro Ala Gln Phe Ala Lys Ala Lys Thr Glu Asn
 44 1 5 10 15
 47 Phe Asp Lys Lys Val Ile Leu Ser Asn Leu Asn Lys Pro His Ala Leu
 48 20 25 30
 51 Leu Trp Gly Pro Asp Asn Gln Ile Trp Leu Thr Glu Arg Ala Thr Gly
 52 35 40 45
 55 Lys Ile Leu Arg Val Asn Pro Val Ser Gly Ser Ala Lys Thr Val Phe
 56 50 55 60
 59 Gln Val Pro Glu Ile Val Ser Asp Ala Asp Gly Gln Asn Gly Leu Leu
 60 65 70 75 80
 63 Gly Phe Ala Phe His Pro Asp Phe Lys His Asn Pro Tyr Ile Tyr Ile
 64 85 90 95
 67 Ser Gly Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn

see p. 7

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71 Gln Thr Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Thr Thr Asp Thr Phe
72      115      120      125
75 Glu Lys Pro Ile Asp Leu Ile Ala Gly Leu Pro Ser Ser Lys Asp His
76      130      135      140
79 Gln Ser Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr
80 145      150      155      160
83 Ile Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
84      165      170      175
87 Gln Ala Gln His Thr Pro Thr Gln Gln Glu Leu Asn Ser Lys Asp Tyr
88      180      185      190
91 His Thr Tyr Met Gly Lys Val Leu Arg Leu Asn Leu Asp Gly Ser Val
92      195      200      205
95 Pro Lys Asp Asn Pro Ser Phe Asn Gly Val Val Ser His Ile Tyr Thr
96      210      215      220
99 Leu Gly His Arg Asn Pro Gln Gly Leu Ala Phe Ala Pro Asn Gly Lys
100 225      230      235      240
103 Leu Leu Gln Ser Glu Gln Gly Pro Asn Ser Asp Asp Glu Ile Asn Leu
104      245      250      255
107 Val Leu Lys Gly Gly Asn Tyr Gly Trp Pro Asn Val Ala Gly Tyr Lys
108      260      265      270
111 Asp Asp Ser Gly Tyr Ala Tyr Ala Asn Tyr Ser Ala Ala Thr Asn Lys
112      275      280      285
115 Ser Gln Ile Lys Asp Leu Ala Gln Asn Gly Ile Lys Val Ala Thr Gly
116      290      295      300
119 Val Pro Val Thr Lys Glu Ser Glu Trp Thr Gly Lys Asn Phe Val Pro
120 305      310      315      320
123 Pro Leu Lys Thr Leu Tyr Thr Val Gln Asp Thr Tyr Asn Tyr Asn Asp
124      325      330      335
127 Pro Thr Cys Gly Glu Met Ala Tyr Ile Cys Trp Pro Thr Val Ala Pro
128      340      345      350
131 Ser Ser Ala Tyr Val Tyr Thr Gly Gly Lys Lys Ala Ile Pro Gly Trp
132      355      360      365
135 Glu Asn Thr Leu Leu Val Pro Ser Leu Lys Arg Gly Val Ile Phe Arg
136      370      375      380
139 Ile Lys Leu Asp Pro Thr Tyr Ser Thr Thr Leu Asp Asp Ala Ile Pro
140 385      390      395      400
143 Met Phe Lys Ser Asn Asn Arg Tyr Arg Asp Val Ile Ala Ser Pro Glu
144      405      410      415
147 Gly Asn Thr Leu Tyr Val Leu Thr Asp Thr Ala Gly Asn Val Gln Lys
148      420      425      430
151 Asp Asp Gly Ser Val Thr His Thr Leu Glu Asn Pro Gly Ser Leu Ile
152      435      440      445
155 Lys Phe Thr Tyr Asn Gly Lys
156      450      455
159 <210> SEQ ID NO: 2
160 <211> LENGTH: 1368
161 <212> TYPE: DNA
162 <213> ORGANISM: Acinetobacter baumannii
164 <400> SEQUENCE: 2

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165 gatatacctc tgacacctgc tcagttcgca aaagcgaaaa cagaaaattt tgataaaaaa 60
167 gtgattctgt ccaatttaaa taaaccacat gctttgttat gggggccaga taatcaaatt 120
169 tggttaaccg aacgtgcaac tggcaaaatt ttaagagtaa atcctgtatc tggtagcgcg 180
171 aaaacagtat ttcaggttcc tgaaattgtg agtgatgctg atgggcaaaa tggtttggtta 240
173 ggttttgctt ttcacctga ctttaaacat aacccttata tctatatttc aggcactttt 300
175 aaaaatccaa aatctacaga taaagagtta cctaatacaga cgattattcg tagatatacc 360
177 tataataaaa ctacagatac atttgaaaag cctattgatt tgattgcagg tttaccgtca 420
179 tcaaaagatc atcagtcagg tcgtctcggt attgggccag accaaaaaat ctactatacg 480
181 attggtgacc aaggtcgtaa tcagttagct tatctgttct taccgaatca ggcacagcat 540
183 actccgactc agcaagagct caatagtaaa gactaccata catatatggg taaagtatta 600
185 cgcttaaatc tggacggcag tgtacctaaa gacaacccaa gctttaacgg cgtagtgagt 660
187 catatctaca ctttagggca ccgtaatcca caaggtttag catttgcccc aaatggaaag 720
189 cttttacaat ctgagcaagg accaaattct gatgatgaaa ttaaccttgt attaaaaggt 780
191 ggtaactatg gctggccaaa tgtagctggg tataaagatg acagtgggta tgcctatgca 840
193 aactattcgg cagcaaccaa taaatcacia attaaagatt tagctcaaaa cgggataaaa 900
195 gtagcaacag gtgttcctgt gactaaagag tctgaatgga ctggtaaaaa ctttgtgccg 960
197 cctttgaaaa ctttatatac ggtacaagat acctataact ataatgaccc tacttgtggg 1020
199 gagatggcat atatttgctg gccaacgggt gcaccgtcat cagcatatgt atatacggga 1080
201 ggcaaaaaag cgattccagg gtgggaaaaat acattattgg tcccatcttt aaaacgtggg 1140
203 gtgattttcc gtattaaatt ggaccgcaga tatagcacga ctttggatga tgctatccca 1200
205 atgttttaaa gcaataaccg ttatcgtgat gtcacgcta gtccagaagg taatacctta 1260
207 tatgtgctga ctgatacagc ggggaatgta caaaaagatg atggttctgt cactcatact 1320
209 ttagagaatc ccggttctct cattaaattt acatataacg gtaagtaa 1368

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212 <210> SEQ ID NO: 3

213 <211> LENGTH: 33

214 <212> TYPE: DNA

215 <213> ORGANISM: Artificial Sequence

217 <220> FEATURE:

218 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide

220 <400> SEQUENCE: 3

221 agtgatgctg atgggaataa tggtttggtta ggt 33

224 <210> SEQ ID NO: 4

225 <211> LENGTH: 33

226 <212> TYPE: DNA

227 <213> ORGANISM: Artificial Sequence

229 <220> FEATURE:

230 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide

232 <400> SEQUENCE: 4

233 agtgatgctg atggggagaa tggtttggtta ggt 33

236 <210> SEQ ID NO: 5

237 <211> LENGTH: 33

238 <212> TYPE: DNA

239 <213> ORGANISM: Artificial Sequence

241 <220> FEATURE:

242 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide

244 <400> SEQUENCE: 5

245 agtgatgctg atgggacaaa tggtttggtta ggt 33

248 <210> SEQ ID NO: 6

249 <211> LENGTH: 33

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Output Set: N:\CRF4\01302007\J570904B.raw

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250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
256 <400> SEQUENCE: 6
257 agtgatgctg atgggatgaa tggtttggtta ggt 33
260 <210> SEQ ID NO: 7
261 <211> LENGTH: 33
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
268 <400> SEQUENCE: 7
269 agtgatgctg atgggggggaa tggtttggtta ggt 33
272 <210> SEQ ID NO: 8
273 <211> LENGTH: 33
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
280 <400> SEQUENCE: 8
281 agtgatgctg atgggaagaa tggtttggtta ggt 33
284 <210> SEQ ID NO: 9
285 <211> LENGTH: 33
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
292 <400> SEQUENCE: 9
293 gaccaaggctc gtaatatattt agcttatctg ttc 33
296 <210> SEQ ID NO: 10
297 <211> LENGTH: 33
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
304 <400> SEQUENCE: 10
305 gaccaaggctc gtaatgtatt agcttatctg ttc 33
308 <210> SEQ ID NO: 11
309 <211> LENGTH: 33
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
316 <400> SEQUENCE: 11
317 gaccaaggctc gtaatgcatt agcttatctg ttc 33
320 <210> SEQ ID NO: 12
321 <211> LENGTH: 43
322 <212> TYPE: DNA

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323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
328 <400> SEQUENCE: 12
329 cgaatcaggc acagcatact ccgactcagc aagagctcaa tag          43
332 <210> SEQ ID NO: 13
333 <211> LENGTH: 45
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Synthetic
340 <220> FEATURE:
341 <221> NAME/KEY: misc_feature
342 <222> LOCATION: (17)..(25)
343 <223> OTHER INFORMATION: "n stands for any base"
346 <400> SEQUENCE: 13
W--> 347 gtaagaacag ataagcnnnn nnnnnacgac cttggtcacc aatcg          45
350 <210> SEQ ID NO: 14
351 <211> LENGTH: 40
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial Sequence
355 <220> FEATURE:
356 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
358 <400> SEQUENCE: 14
359 gatgctgatg ggcaaaatgg tttgtaggt tttgcttttc          40
362 <210> SEQ ID NO: 15
363 <211> LENGTH: 38
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial Sequence
367 <220> FEATURE:
368 <223> OTHER INFORMATION: Synthetic
370 <220> FEATURE:
371 <221> NAME/KEY: misc_feature
372 <222> LOCATION: (7)..(15)
373 <223> OTHER INFORMATION: "n stands for any base"
376 <400> SEQUENCE: 15
W--> 377 actcacnnnn nnnnnaacct gaaatactgt tttcgcgc          38
380 <210> SEQ ID NO: 16
381 <211> LENGTH: 50
382 <212> TYPE: DNA
383 <213> ORGANISM: Artificial Sequence
385 <220> FEATURE:
386 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
388 <400> SEQUENCE: 16
389 tttaccgtca tcaaaagatc atcagtctgg tcgtctcggt attggtccag          50
392 <210> SEQ ID NO: 17
393 <211> LENGTH: 52
394 <212> TYPE: DNA
395 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY
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3rd.txt



Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 17,18,19,20,21,22,23,24,25
Seq#:15; N Pos. 7,8,9,10,11,12,13,14,15
Seq#:17; N Pos. 18,19,20,21,22,23,24,25,26
Seq#:19; N Pos. 16,17,18,19,20,21,22,23,24
Seq#:21; N Pos. 17,18,19
Seq#:30; N Pos. 16
Seq#:33; N Pos. 16
Seq#:34; N Pos. 16
Seq#:49; N Pos. 17
Seq#:58; N Pos. 17
Seq#:60; N Pos. 17
Seq#:61; N Pos. 17
Seq#:62; N Pos. 17
Seq#:63; N Pos. 17
Seq#:69; N Pos. 19,20
Seq#:70; N Pos. 19,20
Seq#:71; N Pos. 19,20
Seq#:73; N Pos. 20,21,22
Seq#:74; N Pos. 20,21,22

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:941 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:0
L:989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0
L:1007 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:0
L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:0
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
L:1139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:0
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73 after pos.:0
L:1185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0